

02-1147.SeqListing.CRF
SEQUENCE LISTING

<110> Tryggvason, Karl
Salo, Sirpa

<120> Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor growth and metastasis

<130> 02-1147-US

<150> 60/422,009

<151> 2002-10-29

<150> US 09/756,071

<151> 2001-01-08

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<170> PatentIn version 3.1

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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665

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02-1147.SeqListing.CRF

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Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
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Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
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Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
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Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
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02-1147.SeqListing.CRF

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 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
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02-1147.SeqListing.CRF

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acc Thr	caa Gln 130	gac Asp	cag Gln	aga Arg	ctg Leu	cta Leu 135	gac Asp	tcc Ser	aag Lys	tgt Cys	gac Asp 140	tgt Cys	gac Asp	cca Pro	gct Ala	549
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02-1147.SeqListing.CRF

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cgc Arg	cct Pro 370	gtc Val	tct Ser	gga Gly	gcc Ala 375	cca Pro	gca Ala	ccc Pro	tgg Trp	gtt Val	gaa Glu 380	cag Gln	tgt Cys	ata Ile	tgt Cys	1269
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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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02-1147.SeqListing.CRF

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Ser	Thr 210	Phe	His	Gln	Asp	Val 215
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02-1147.SeqListing.CRF

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 Lys Arg Asp Ser Ala 405 Arg Leu Gly Pro Phe 410 Gly Thr Cys Ile Pro 415 Cys
 Asn Cys Gln Gly 420 Gly Gly Ala Cys Asp 425 Pro Asp Thr Gly Asp 430 Cys Tyr
 Ser Gly Asp 435 Glu Asn Pro Asp Ile 440 Glu Cys Ala Asp Cys 445 Pro Ile Gly
 Phe Tyr 450 Asn Asp Pro His Asp 455 Pro Arg Ser Cys Lys 460 Pro Cys Pro Cys
 His 465 Asn Gly Phe Ser Cys 470 Ser Val Ile Pro Glu 475 Thr Glu Glu Val Val 480
 Cys Asn Asn Cys Pro 485 Pro Gly Val Thr Gly 490 Ala Arg Cys Glu Leu 495 Cys
 Ala Asp Gly Tyr 500 Phe Gly Asp Pro Phe 505 Gly Glu His Gly Pro 510 Val Arg
 Pro Cys Gln 515 Pro Cys Gln Cys Asn 520 Ser Asn Val Asp Pro 525 Ser Ala Ser
 Gly Asn 530 Cys Asp Arg Leu Thr 535 Gly Arg Cys Leu Lys 540 Cys Ile His Asn
 Thr 545 Ala Gly Ile Tyr Cys 550 Asp Gln Cys Lys Ala 555 Gly Tyr Phe Gly Asp 560
 Pro Leu Ala Pro Asn 565 Pro Ala Asp Lys Cys 570 Arg Ala Cys Asn Cys 575 Asn

02-1147.SeqListing.CRF

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

02-1147.SeqListing.CRF

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
1010 1015 1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
1025 1030 1035

Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
1040 1045 1050

Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
1055 1060 1065

Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys

1070

1075

1080

Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
 1085 1090 1095

Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Gly Met
 1100 1105 1110

<210> 5
 <211> 530
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Portion of Domain III of laminin gamma 2

<400> 5
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 gttattcagg ggatgagaat cctgacattg agtgtgctga ctgcccaatt ggtttctaca 180
 acgatccgca cgacccccgc agctgcaagc catgtccctg tcataacggg ttcagctgct 240
 cagtgtattcc ggagacggag gaggtggtgt gcaataactg ccctcccggg gtcaccggtg 300
 cccgctgtga gctctgtgct gatggctact ttggggaccc ctttggtgaa catggcccag 360
 tgaggccttg tcagccctgt caatgcaaca gcaatgtgga cccagtgcc tctgggaatt 420
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 accagtgcaa agcaggctac ttcggggacc cattggctcc caaccagca 530

<210> 6
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Portion of Domain III of laminin gamma 2.

<400> 6

Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg
 1 5 10 15

Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly
 20 25 30

Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro
 35 40 45

02-1147.SeqListing.CRF

Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro His
50 55 60

Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser Cys
65 70 75 80

Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Pro
85 90 95

Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly
100 105 110

Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys Gln
115 120 125

Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu
130 135 140

Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr Cys
145 150 155 160

Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn Pro
165 170 175

Ala

<210> 7
<211> 681
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2

<400> 7
tgtatatgtc ctgttgggta caaggggcaa ttctgccagg attgtgcttc tggctacaag 60
agagattcag cgagactggg gccttttggc acctgtattc cttgtaactg tcaaggggga 120
ggggcctgtg atccagacac aggagattgt tattcagggg atgagaatcc tgacattgag 180
tgtgctgact gcccaattgg tttctacaac gatccgcacg acccccgcag ctgcaagcca 240
tgtccctgtc ataacgggtt cagctgtca gtgattccgg agacggagga ggtggtgtgc 300
aataactgcc ctcccggggt caccggtgcc cgctgtgagc tctgtgctga tggctacttt 360
ggggaccctt ttggtgaaca tggcccagtg aggccttgtc agccctgtca atgcaacagc 420

02-1147.SeqListing.CRF

aatgtggacc ccagtgcctc tgggaattgt gaccggctga caggcagggtg tttgaagtgt	480
atccacaaca cagccggcat ctactgcgac cagtgcaaag caggctactt cggggaccca	540
ttggctccca acccagcaga caagtgtcga gcttgcaact gtaaccccat gggctcagag	600
cctgtaggat gtcgaagtga tggcacctgt gtttgcaagc caggatttgg tggccccaac	660
tgtgagcatg gagcattcag c	681

<210> 8
 <211> 227
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Complete domain III of laminin gamma 2.

<400> 8

Cys Ile Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala	1	5	10	15
Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys	20	25	30	
Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly	35	40	45	
Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys	50	55	60	
Pro Ile Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro	65	70	75	80
Cys Pro Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu	85	90	95	
Glu Val Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys	100	105	110	
Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly	115	120	125	
Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro	130	135	140	
Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys	145	150	155	160

02-1147.SeqListing.CRF

Ile His Asn Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr
165 170 175

Phe Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys
180 185 190

Asn Cys Asn Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly
195 200 205

Thr Cys Val Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly
210 215 220

Ala Phe Ser
225

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> N-terminal portion of domain III of laminin gamma 2.

<400> 9

Cys Ile Cys Pro Val Gly Tyr Lys Gly
1 5

<210> 10
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> C-terminal portion of domain III of laminin gamma 2.

<400> 10

Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu Pro Val
1 5 10 15

Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
20 25 30

Pro Asn Cys Glu His Gly Ala Phe Ser
35 40